



SEQUENCE LISTING

<110> Matuschek, Markus
Heinekamp, Thorsten
Schmidt, Andre
Brakhage, Axel

<120> Method for the genetic modification of organisms of the genus
Blakeslea, corresponding organisms, and the use of the same

<130> 13311-00010-US

<140> US 10/541,993
<141> 2005-07-08

<150> PCT/EP2004/000100
<151> 2004-01-09

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Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp	
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Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro	
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Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile	
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Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His	
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Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp	
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Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
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Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
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His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
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Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
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Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
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Met His Val
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Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser
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Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly
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Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro
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aaa gac cct gac ttc cac aag gga aat ccc ggc ctt gtc ccc tgg ttc Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe 180 185 190 195			752
gcc agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu 200 205 210			800
gca tgg tgg gca gtg gtg atg caa atg ctg ggg gcg ccc atg gca aat Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn 215 220 225			848
ctc cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu 230 235 240			896
ttc tac ttc ggc act tac ctg cca cac aag cct gag cca ggc cct gca Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala 245 250 255			944
gca ggc tct cag gtg atg gcc tgg ttc agg gcc aag aca agt gag gca Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala 260 265 270 275			992
tct gat gtg atg agt ttc ctg aca tgc tac cac ttt gac ctg cac tgg Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp 280 285 290			1040
gag cac cac agg tgg ccc ttt gcc ccc tgg tgg cag ctg ccc cac tgc Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys 295 300 305			1088
cgc cgc ctg tcc ggg cgt ggc ctg gtg cct gcc ttg gca tga Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala 310 315 320			1130
cctgggtccct ccgctggtga cccagcgtct gcacaagagt gtcattgctac aggggtgctgc			1190
ggccagtggc agcgcagtgc actctcagcc tgtatggggc taccgctgtg ccactgagca			1250

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ctgggcatgc cactgagcac tgggcgtgct actgagcaat gggcgtgcta ctgagcaatg 1310
ggcgtgctac tgacaatggg cgtgctactg gggctctggca gtggctagga tggagtttga 1370
tgcattcagt agcgggtggcc aacgtcatgt ggatgggtgga agtgctgagg ggtttaggca 1430
gccggcattt gagagggcta agttataaat cgcattgctgc tcatgcgcac atatctgcac 1490
acagccaggg aaatcccttc gagagtgatt atgggacact tgtattgggt tcgtgctatt 1550
gtttttattca gcagcagtac ttagtgaggg tgagagcagg gtggtgagag tggagtgagt 1610
gagtatgaac ctggtcagcg aggtgaacag cctgtaatga atgactctgt ct 1662

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<210> 14
<211> 320
<212> PRT
<213> Haematococcus pluvialis

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<400> 14

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Met His Val Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala
1          5          10          15

```

```

Ala Ala Ser Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His
20          25          30

```

```

Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala
35          40          45

```

```

Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
50          55          60

```

```

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile
65          70          75          80

```

```

Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
85          90          95

```

```

Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala
100          105          110

```

```

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr
115          120          125

```

```

Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu
130          135          140

```

```

Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp
145          150          155          160

```

Tyr Ser Met Leu His Arg Lys His Trp Glu His His Asn His Thr Gly
 165 170 175

Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val
 180 185 190

Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe
 195 200 205

Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro
 210 215 220

Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala
 225 230 235 240

Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro
 245 250 255

Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr
 260 265 270

Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp
 275 280 285

Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu
 290 295 300

Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala
 305 310 315 320

<210> 15
 <211> 729
 <212> DNA
 <213> Agrobacterium aurantiacum

<220>
 <221> CDS
 <222> (1)..(729)

<400> 15
 atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc acc agc ctg
 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15 48

atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat
 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30 96

gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca 144
Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
35 40 45

aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg 192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
50 55 60

cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat 240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65 70 75 80

gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg 288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc 336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
100 105 110

gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc 384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc 432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac 480
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc 528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg 576
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg 624
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac 672
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac 720
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225 230 235 240

acc gca tga 729
Thr Ala

<210> 16
<211> 242
<212> PRT
<213> Agrobacterium aurantiacum

<400> 16

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
 35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
 225 230 235 240

<400> 17																		
ctgcaggccg	ggcccgggtg	ccaatggtcg	caaccggcag	gactggaaca	ggacggcggg												60	
ccgggtctagg	ctgtcgccct	acgcagcagg	agtttcgg	atg tcc gga cgg aag cct													116	
				Met	Ser	Gly	Arg	Lys	Pro									
				1								5						
ggc aca act	ggc gac acg	atc gtc aat	ctc ggt ctg	acc gcc gcg atc													164	
Gly Thr Thr	Gly Asp Thr	Ile Val Asn	Leu Gly Leu	Thr Ala Ala Ile														
				10								15						
ctg ctg tgc	tgg ctg gtc	ctg cac gcc	ttt acg cta	tgg ttg cta gat													212	
Leu Leu Cys	Trp Leu Val	Leu His Ala	Phe Thr Leu	Trp Leu Leu Asp														
				25								30						
gcg gcc gcg	cat ccg ctg	ctt gcc gtg	ctg tgc ctg	gct ggg ctg acc													260	
Ala Ala Ala	His Pro Leu	Leu Ala Val	Leu Cys Leu	Ala Gly Leu Thr														
				40								45						
tgg ctg tcg	gtc ggg ctg	ttc atc atc	gcg cat gac	gca atg cac ggg													308	
Trp Leu Ser	Val Gly Leu	Phe Ile Ile	Ala His Asp	Ala Met His Gly														
				60								65						
tcc gtg gtg	ccg ggg cgg	ccg cgc gcc	aat gcg gcg	atc ggg caa ctg													356	
Ser Val Val	Pro Gly Arg	Pro Arg Ala	Asn Ala Ala	Ile Gly Gln Leu														
				75								80						
gcg ctg tgg	ctc tat gcg	ggg ttc tcg	tgg ccc aag	ctg atc gcc aag													404	
Ala Leu Trp	Leu Tyr Ala	Gly Phe Ser	Trp Pro Lys	Leu Ile Ala Lys														
				90								95						
cac atg acg	cat cac cgg	cac gcc ggc	acc gac aac	gat ccc gat ttc													452	
His Met Thr	His His Arg	His Ala Gly	Thr Asp Asn	Asp Pro Asp Phe														
				105								110						
ggg cac gga	ggg ccc gtg	cgc tgg tac	ggc agc ttc	gtc tcc acc tat													500	
Gly His Gly	Gly Pro Val	Arg Trp Tyr	Gly Ser Phe	Val Ser Thr Tyr														
				120								125						
ttc ggc tgg	cga gag gga	ctg ctg cta	ccg gtg atc	gtc acc acc tat													548	
Phe Gly Trp	Arg Glu Gly	Leu Leu Leu	Pro Val Ile	Val Thr Thr Tyr														
				135								140						
gcg ctg atc	ctg ggc gat	cgc tgg atg	tat gtc atc	ttc tgg ccg gtc													596	
Ala Leu Ile	Leu Gly Asp	Arg Trp Met	Tyr Val Ile	Phe Trp Pro Val														

155	160	165	
ccg gcc gtt ctg gcg tcg atc cag att ttc gtc ttc gga act tgg ctg			644
Pro Ala Val Leu Ala Ser Ile Gln Ile Phe Val Phe Gly Thr Trp Leu			
170	175	180	
ccc cac cgc ccg gga cat gac gat ttt ccc gac cgg cac aac gcg agg			692
Pro His Arg Pro Gly His Asp Asp Phe Pro Asp Arg His Asn Ala Arg			
185	190	195	
tcg acc ggc atc ggc gac ccg ttg tca cta ctg acc tgc ttc cat ttc			740
Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu Leu Leu Thr Cys Phe His Phe			
200	205	210	
ggc ggc tat cac cac gaa cat cac ctg cat ccg cat gtg ccg tgg tgg			788
Gly Gly Tyr His His Glu His His Leu His Pro His Val Pro Trp Trp			
215	220	225	230
cgc ctg cct cgt aca cgc aag acc gga ggc cgc gca tga cgcaattcct			837
Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly Arg Ala			
235	240		
cattgtcgtg ggcacagtcc tcgtgatgga gctgaccgcc tattccgtcc accgctggat			897
tatgcacggc ccctaggct ggggctggca caagtcccat cacgaagagc acgaccacgc			957
gttggaagaag aacgacctct acggcgtcgt cttcgcggtg ctggcgacga tcctcttcac			1017
cgtgggcgcc tattggtggc cgggtgctgtg gtggatcgcc ctgggcatga cggctctatgg			1077
gttgatctat ttcatcctgc acgacgggct tgtgcatcaa cgctggccgt ttcggtatat			1137
tccgcggcgg ggcattttcc gcaggctcta ccaagctcat cgcctgcacc acgcggtcga			1197
ggggcgggac cactgcgtca gcttcggcct catctatgcc ccacccgtgg acaagctgaa			1257
gcaggatctg aagcggtcgg gtgtcctgcg cccccaggac gagcgtccgt cgtgatctct			1317
gatcccgcg tggccgcatg aaatccgacg tgctgctggc aggggcggc cttgccaacg			1377
gactgatcgc gctggcgatc cgcaaggcgc ggcccgaact tcgcgtgctg ctgctggacc			1437
gtgcggcggg cgctcggac gggcatactt ggtcctgcca cgacaccgat ttggcgccgc			1497
actggctgga ccgcctgaag ccgatcaggc gtggcgactg gcccgatcag gaggtgcggt			1557
tcccagacca ttgcgaagg ctccgggccg gatatggctc gatcgacggg cgggggctga			1617
tgcgtgcggt gacc			1631

<210> 18
 <211> 242
 <212> PRT
 <213> Alcaligenes sp.

<400> 18

Met	Ser	Gly	Arg	Lys	Pro	Gly	Thr	Thr	Gly	Asp	Thr	Ile	Val	Asn	Leu
1				5					10					15	

Gly Leu Thr Ala Ala Ile Leu Leu Cys Trp Leu Val Leu His Ala Phe
 20 25 30

Thr Leu Trp Leu Leu Asp Ala Ala Ala His Pro Leu Leu Ala Val Leu
 35 40 45

Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr
 100 105 110

Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly
 115 120 125

Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly
 225 230 235 240

Arg Ala

<210> 19
 <211> 729
 <212> DNA
 <213> *Paracoccus marcusii*

<220>
 <221> CDS
 <222> (1) .. (729)

<400> 19
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 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15

atc gtc tcg ggc ggc atc atc gcc gca tgg ctg gcc ctg cat gtg cat 96
 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

gcg ctg tgg ttt ctg gac gcg gcg gcc cat ccc atc ctg gcg gtc gcg 144
 Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala
 35 40 45

aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg 192
 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

cat gac gcg atg cac ggg tcg gtc gtg ccg ggg cgt ccg cgc gcc aat 240
 His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg 288
 Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc 336
 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

gac gac gac cca gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc 384
 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc 432
 Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

gtc atc gtg acg gtc tat gcg ctg atc ctg ggg gat cgc tgg atg tac 480
 Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

gtg gtc ttc tgg ccg ttg ccg tcg atc ctg gcg tcg atc cag ctg ttc 528
 Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

gtg ttc ggc act tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg 576
 Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

gac cgc cat aat gcg cgg tcg tcg cgg atc agc gac cct gtg tcg ctg 624
 Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu

195	200	205	
ctg acc tgc ttt cat ttt ggc ggt tat cat cac gaa cac cac ctg cac			672
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His			
210	215	220	
ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac			720
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp			
225	230	235	240
acc gca tga			729
Thr Ala			

<210> 20
 <211> 242
 <212> PRT
 <213> *Paracoccus marcusii*

<400> 20

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
1 5 10 15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala
35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
 225 230 235 240

Thr Ala

<210> 21
 <211> 1629
 <212> DNA
 <213> Synechocystis sp.

<220>
 <221> CDS
 <222> (1)..(1629)

<400> 21
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 Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu
 1 5 10 15
 gtc tgt gca gcc tat ttg ctc caa cgg ggc ttg ggg gtg acg tta cta 96
 Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu
 20 25 30
 gaa aag cgg gaa gta cca ggg ggg gcg gcc acc aca gaa gct ctc atg 144
 Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met
 35 40 45
 ccg gag cta tcc ccc cag ttt cgc ttt aac cgc tgt gcc att gac cac 192
 Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
 50 55 60
 gaa ttt atc ttt ctg ggg ccg gtg ttg cag gag cta aat tta gcc cag 240
 Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
 65 70 75 80
 tat ggt ttg gaa tat tta ttt tgt gac ccc agt gtt ttt tgt ccg ggg 288
 Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
 85 90 95
 ctg gat ggc caa gct ttt atg agc tac cgt tcc cta gaa aaa acc tgt 336

Leu	Asp	Gly	Gln	Ala	Phe	Met	Ser	Tyr	Arg	Ser	Leu	Glu	Lys	Thr	Cys	
			100					105					110			
gcc	cac	att	gcc	acc	tat	agc	ccc	cga	gat	gcg	gaa	aaa	tat	cgg	caa	384
Ala	His	Ile	Ala	Thr	Tyr	Ser	Pro	Arg	Asp	Ala	Glu	Lys	Tyr	Arg	Gln	
		115					120					125				
ttt	gtc	aat	tat	tgg	acg	gat	ttg	ctc	aac	gct	gtc	cag	cct	gct	ttt	432
Phe	Val	Asn	Tyr	Trp	Thr	Asp	Leu	Leu	Asn	Ala	Val	Gln	Pro	Ala	Phe	
		130				135					140					
aat	gct	ccg	ccc	cag	gct	tta	cta	gat	tta	gcc	ctg	aac	tat	ggg	tgg	480
Asn	Ala	Pro	Pro	Gln	Ala	Leu	Leu	Asp	Leu	Ala	Leu	Asn	Tyr	Gly	Trp	
145					150					155					160	
gaa	aac	tta	aaa	tcc	gtg	ctg	gcg	atc	gcc	ggg	tcg	aaa	acc	aag	gcg	528
Glu	Asn	Leu	Lys	Ser	Val	Leu	Ala	Ile	Ala	Gly	Ser	Lys	Thr	Lys	Ala	
				165				170						175		
ttg	gat	ttt	atc	cgc	act	atg	atc	ggc	tcc	ccg	gaa	gat	gtg	ctc	aat	576
Leu	Asp	Phe	Ile	Arg	Thr	Met	Ile	Gly	Ser	Pro	Glu	Asp	Val	Leu	Asn	
			180					185					190			
gaa	tgg	ttc	gac	agc	gaa	cgg	gtt	aaa	gct	cct	tta	gct	aga	cta	tgt	624
Glu	Trp	Phe	Asp	Ser	Glu	Arg	Val	Lys	Ala	Pro	Leu	Ala	Arg	Leu	Cys	
		195					200					205				
tcg	gaa	att	ggc	gct	ccc	cca	tcc	caa	aag	ggg	agt	agc	tcc	ggc	atg	672
Ser	Glu	Ile	Gly	Ala	Pro	Pro	Ser	Gln	Lys	Gly	Ser	Ser	Ser	Gly	Met	
	210					215					220					
atg	atg	gtg	gcc	atg	cgg	cat	ttg	gag	gga	att	gcc	aga	cca	aaa	gga	720
Met	Met	Val	Ala	Met	Arg	His	Leu	Glu	Gly	Ile	Ala	Arg	Pro	Lys	Gly	
225					230					235					240	
ggc	act	gga	gcc	ctc	aca	gaa	gcc	ttg	gtg	aag	tta	gtg	caa	gcc	caa	768
Gly	Thr	Gly	Ala	Leu	Thr	Glu	Ala	Leu	Val	Lys	Leu	Val	Gln	Ala	Gln	
				245					250					255		
ggg	gga	aaa	atc	ctc	act	gac	caa	acc	gtc	aaa	cgg	gta	ttg	gtg	gaa	816
Gly	Gly	Lys	Ile	Leu	Thr	Asp	Gln	Thr	Val	Lys	Arg	Val	Leu	Val	Glu	
			260					265					270			
aac	aac	cag	gcg	atc	ggg	gtg	gag	gta	gct	aac	gga	gaa	cag	tac	cgg	864
Asn	Asn	Gln	Ala	Ile	Gly	Val	Glu	Val	Ala	Asn	Gly	Glu	Gln	Tyr	Arg	
		275					280					285				
gcc	aaa	aaa	ggc	gtg	att	tct	aac	atc	gat	gcc	cgc	cgt	tta	ttt	ttg	912
Ala	Lys	Lys	Gly	Val	Ile	Ser	Asn	Ile	Asp	Ala	Arg	Arg	Leu	Phe	Leu	
	290					295					300					
caa	ttg	gtg	gaa	ccg	ggg	gcc	cta	gcc	aag	gtg	aat	caa	aac	cta	ggg	960
Gln	Leu	Val	Glu	Pro	Gly	Ala	Leu	Ala	Lys	Val	Asn	Gln	Asn	Leu	Gly	
305					310					315					320	
gaa	cga	ctg	gaa	cgg	cgc	act	gtg	aac	aat	aac	gaa	gcc	att	tta	aaa	1008
Glu	Arg	Leu	Glu	Arg	Arg	Thr	Val	Asn	Asn	Asn	Glu	Ala	Ile	Leu	Lys	
				325					330					335		
atc	gat	tgt	gcc	ctc	tcc	ggg	tta	ccc	cac	ttc	act	gcc	atg	gcc	ggg	1056
Ile	Asp	Cys	Ala	Leu	Ser	Gly	Leu	Pro	His	Phe	Thr	Ala	Met	Ala	Gly	

340	345	350	
ccg gag gat cta acg gga act att ttg att gcc gac tcg gta cgc cat			1104
Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His			
355	360	365	
gtc gag gaa gcc cac gcc ctc att gcc ttg ggg caa att ccc gat gct			1152
Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala			
370	375	380	
aat ccg tct tta tat ttg gat att ccc act gta ttg gac ccc acc atg			1200
Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met			
385	390	395	400
gcc ccc cct ggg cag cac acc ctc tgg atc gaa ttt ttt gcc ccc tac			1248
Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr			
405	410	415	
cgc atc gcc ggg ttg gaa ggg aca ggg tta atg ggc aca ggt tgg acc			1296
Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr			
420	425	430	
gat gag tta aag gaa aaa gtg gcg gat cgg gtg att gat aaa tta acg			1344
Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr			
435	440	445	
gac tat gcc cct aac cta aaa tct ctg atc att ggt cgc cga gtg gaa			1392
Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu			
450	455	460	
agt ccc gcc gaa ctg gcc caa cgg ctg gga agt tac aac ggc aat gtc			1440
Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val			
465	470	475	480
tat cat ctg gat atg agt ttg gac caa atg atg ttc ctc cgg cct cta			1488
Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu			
485	490	495	
ccg gaa att gcc aac tac caa acc ccc atc aaa aat ctt tac tta aca			1536
Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr			
500	505	510	
ggg gcg ggt acc cat ccc ggt ggc tcc ata tca ggt atg ccc ggt aga			1584
Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg			
515	520	525	
aat tgc gct cgg gtc ttt tta aaa caa caa cgt cgt ttt tgg taa			1629
Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp			
530	535	540	

<210> 22
 <211> 542
 <212> PRT
 <213> Synechocystis sp.

<400> 22

Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu
1 5 10 15

Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu
 20 25 30

Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met
 35 40 45

Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
 50 55 60

Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
 65 70 75 80

Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
 85 90 95

Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys
 100 105 110

Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
 115 120 125

Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
 130 135 140

Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp
 145 150 155 160

Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala
 165 170 175

Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn
 180 185 190

Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys
 195 200 205

Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met
 210 215 220

Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly
 225 230 235 240

Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln
 245 250 255

Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu
260 265 270

Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg
275 280 285

Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu
290 295 300

Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly
305 310 315 320

Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys
325 330 335

Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly
340 345 350

Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His
355 360 365

Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala
370 375 380

Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met
385 390 395 400

Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr
405 410 415

Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
420 425 430

Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
435 440 445

Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
450 455 460

Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
465 470 475 480

Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
485 490 495

Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr

500	505	510
Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg		
515	520	525

Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp
530 535 540

<210> 23
 <211> 776
 <212> DNA
 <213> Bradyrhizobium sp.

<220>
 <221> CDS
 <222> (1)..(774)

<400> 23	
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Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg	
1 5 10 15	
gac gat gcg agg cag cgc cgc gtc ggt ctc acg ctg gcc gcg gtc atc	96
Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile	
20 25 30	
atc gcc gcc tgg ctg gtg ctg cat gtc ggt ctg atg ttc ttc tgg ccg	144
Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro	
35 40 45	
ctg acc ctt cac agc ctg ctg ccg gct ttg cct ctg gtg gtg ctg cag	192
Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln	
50 55 60	
acc tgg ctc tat gta ggc ctg ttc atc atc gcg cat gac tgc atg cac	240
Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His	
65 70 75 80	
ggc tcg ctg gtg ccg ttc aag ccg cag gtc aac cgc cgt atc gga cag	288
Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln	
85 90 95	
ctc tgc ctg ttc ctc tat gcc ggg ttc tcc ttc gac gct ctc aat gtc	336
Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val	
100 105 110	
gag cac cac aag cat cac cgc cat ccc ggc acg gcc gag gat ccc gat	384
Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp	
115 120 125	
ttc gac gag gtg ccg ccg cac ggc ttc tgg cac tgg ttc gcc agc ttt	432
Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe	
130 135 140	
ttc ctg cac tat ttc ggc tgg aag cag gtc gcg atc atc gca gcc gtc	480
Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val	
145 150 155 160	

tgc	ctg	gtt	tat	cag	ctc	gtc	ttc	gcc	gtt	ccc	ttg	cag	aac	atc	ctg	528
Ser	Leu	Val	Tyr	Gln	Leu	Val	Phe	Ala	Val	Pro	Leu	Gln	Asn	Ile	Leu	
				165					170					175		

ctg ttc tgg gcg ctg ccc ggg ctg ctg tcg gcg ctg cag ctg ttc acc 576
Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
180 185 190

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ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccc ttc gcc gat      624
Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
          195                      200                      205

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cgc cac aac gcg cgg acg agc gaa ttt ccc gcg tgg ctg tcg ctg ctg 672
Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
210 215 220

acc tgc ttc cac ttc ggc ttt cat cac gag cat cat ctg cat ccc gat 720
Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
225 230 235 240

gcg ccg tgg tgg cgg ctg ccg gag atc aag cgg cgg gcc ctg gaa agg 768
Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
245 250 255

cgt gac ta	776
Arg Asp	

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<210> 24
<211> 258
<212> PRT
<213> Bradyrhizobium sp.
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<400> 24

Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg
1 5 10 15

Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
20 25 30

Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
35 40 45

Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
50 55 60

Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
65 70 75 80

Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
85 90 95

Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
 100 105 110

Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
 115 120 125

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
 130 135 140

Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
 145 150 155 160

Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
 165 170 175

Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
 180 185 190

Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
 195 200 205

Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
 210 215 220

Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
 225 230 235 240

Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
 245 250 255

Arg Asp

<210> 25
 <211> 777
 <212> DNA
 <213> Nostoc sp.

<220>
 <221> CDS
 <222> (1)..(777)

<400> 25
 atg gtt cag tgt caa cca tca tct ctg cat tca gaa aaa ctg gtg tta 48
 Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
 1 5 10 15

ttg tca tcg aca atc aga gat gat aaa aat att aat aag ggt ata ttt 96
 Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe

tct tta taa 777
Ser Leu

<210> 26
 <211> 258
 <212> PRT
 <213> Nostoc sp.

<400> 26

Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
 1 5 10 15

Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
 20 25 30

Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45

Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
 50 55 60

Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80

Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 100 105 110

Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125

Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
 130 135 140

Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160

Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu
 165 170 175

Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
 180 185 190

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
 195 200 205

Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
 210 215 220

Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His
 225 230 235 240

Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile
 245 250 255

Ser Leu

<210> 27
 <211> 789
 <212> DNA
 <213> Nostoc punctiforme

<220>
 <221> CDS
 <222> (1)..(789)

<400> 27
 ttg aat ttt tgt gat aaa cca gtt agc tat tat gtt gca ata gag caa 48
 Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln
 1 5 10 15
 tta agt gct aaa gaa gat act gtt tgg ggg ctg gtg att gtc ata gta 96
 Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
 20 25 30
 att att agt ctt tgg gta gct agt ttg gct ttt tta cta gct att aat 144
 Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
 35 40 45
 tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa 192
 Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
 50 55 60
 atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat 240
 Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
 65 70 75 80
 ggg tca gtt tat cgt aaa aat ccc aaa att aat aat ttt atc ggt tca 288
 Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
 85 90 95
 cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag 336
 Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
 100 105 110
 aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat 384
 Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
 115 120 125
 ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc 432
 Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe

130	135	140	
atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta			480
Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu			
145	150	155	160
ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc			528
Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile			
	165	170	175
tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat			576
Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr			
	180	185	190
ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat			624
Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr			
	195	200	205
ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc			672
Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile			
	210	215	220
gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat			720
Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His			
	225	230	235
gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac			768
Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn			
	245	250	255
aat tca gta acc aat tcg taa			789
Asn Ser Val Thr Asn Ser			
	260		

<210> 28
 <211> 262
 <212> PRT
 <213> Nostoc punctiforme

<400> 28

Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln	
1	15
Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val	
20	30
Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn	
35	45
Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln	
50	60
Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His	
65	80

Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
 85 90 95

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
 100 105 110

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
 115 120 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
 130 135 140

Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
 145 150 155 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
 165 170 175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
 180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
 195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
 210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
 245 250 255

Asn Ser Val Thr Asn Ser
 260

<210> 29
 <211> 762
 <212> DNA
 <213> Nostoc punctiforme

<220>
 <221> CDS
 <222> (1)..(762)

<400> 29
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Val 1	Ile	Gln	Leu 5	Glu	Gln	Pro	Leu	Ser 10	His	Gln	Ala	Lys	Leu 15	Thr	Pro	
gta	ctg	aga	agt	aaa	tct	cag	ttt	aag	ggg	ctt	ttc	att	gct	att	gtc	96
Val	Leu	Arg	Ser 20	Lys	Ser	Gln	Phe	Lys 25	Gly	Leu	Phe	Ile	Ala 30	Ile	Val	
att	gtt	agc	gca	tgg	gtc	att	agc	ctg	agt	tta	tta	ctt	tcc	ctt	gac	144
Ile	Val	Ser 35	Ala	Trp	Val	Ile	Ser 40	Leu	Ser	Leu	Leu	Leu	Ser 45	Leu	Asp	
atc	tca	aag	cta	aaa	ttt	tgg	atg	tta	ttg	cct	gtt	ata	cta	tgg	caa	192
Ile	Ser	Lys 50	Leu	Lys	Phe	Trp 55	Met	Leu	Leu	Pro	Val 60	Ile	Leu	Trp	Gln	
aca	ttt	tta	tat	acg	gga	tta	ttt	att	aca	tct	cat	gat	gcc	atg	cat	240
Thr	Phe	Leu	Tyr	Thr	Gly 70	Leu	Phe	Ile	Thr	Ser 75	His	Asp	Ala	Met	His 80	
ggc	gta	gta	ttt	ccc	caa	aac	acc	aag	att	aat	cat	ttg	att	gga	aca	288
Gly	Val	Val	Phe 85	Pro	Gln	Asn	Thr	Lys 90	Ile	Asn	His	Leu	Ile 95	Gly	Thr	
ttg	acc	cta	tcc	ctt	tat	ggg	ctt	tta	cca	tat	caa	aaa	cta	ttg	aaa	336
Leu	Thr	Leu 100	Ser	Leu	Tyr	Gly	Leu	Leu 105	Pro	Tyr	Gln	Lys	Leu 110	Leu	Lys	
aaa	cat	tgg	tta	cac	cac	cac	aat	cca	gca	agc	tca	ata	gac	ccg	gat	384
Lys	His	Trp 115	Leu	His	His	His	Asn 120	Pro	Ala	Ser	Ser	Ile 125	Asp	Pro	Asp	
ttt	cac	aat	ggg	aaa	cac	caa	agt	ttc	ttt	gct	tgg	tat	ttt	cat	ttt	432
Phe	His	Asn 130	Gly	Lys	His	Gln 135	Ser	Phe	Phe	Ala	Trp 140	Tyr	Phe	His	Phe	
atg	aaa	ggg	tac	tgg	agt	tgg	ggg	caa	ata	att	gcg	ttg	act	att	att	480
Met	Lys	Gly	Tyr	Trp	Ser 150	Trp	Gly	Gln	Ile	Ile 155	Ala	Leu	Thr	Ile	Ile 160	
tat	aac	ttt	gct	aaa	tac	ata	ctc	cat	atc	cca	agt	gat	aat	cta	act	528
Tyr	Asn	Phe	Ala 165	Lys	Tyr	Ile	Leu	His 170	Ile	Pro	Ser	Asp	Asn	Leu 175	Thr	
tac	ttt	tgg	gtg	cta	ccc	tcg	ctt	tta	agt	tca	tta	caa	tta	ttc	tat	576
Tyr	Phe	Trp 180	Val	Leu	Pro	Ser	Leu	Leu 185	Ser	Ser	Leu	Gln	Leu 190	Phe	Tyr	
ttt	ggg	act	ttt	tta	ccc	cat	agt	gaa	cca	ata	ggg	ggg	tat	gtt	cag	624
Phe	Gly	Thr 195	Phe	Leu	Pro	His 200	Ser	Glu	Pro	Ile	Gly	Gly 205	Tyr	Val	Gln	
cct	cat	tgt	gcc	caa	aca	att	agc	cgt	cct	att	tgg	tgg	tca	ttt	atc	672
Pro	His	Cys 210	Ala	Gln	Thr	Ile 215	Ser	Arg	Pro	Ile	Trp 220	Trp	Ser	Phe	Ile	
acg	tgc	tat	cat	ttt	ggc	tac	cac	gag	gaa	cat	cac	gaa	tat	cct	cat	720
Thr	Cys	Tyr	His	Phe	Gly 225	Tyr	His	Glu	Glu	His 235	His	Glu	Tyr	Pro 240	His	
att	tct	tgg	tgg	cag	tta	cca	gaa	att	tac	aaa	gca	aaa	tag			762
Ile	Ser	Trp	Trp	Gln	Leu	Pro	Glu	Ile	Tyr	Lys	Ala	Lys				

245

250

<210> 30
 <211> 253
 <212> PRT
 <213> Nostoc punctiforme

<400> 30

Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro
 1 5 10 15

Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
 20 25 30

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp
 35 40 45

Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
 50 55 60

Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
 65 70 75 80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
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Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
 100 105 110

Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
 115 120 125

Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
 130 135 140

Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
 145 150 155 160

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
 165 170 175

Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
 180 185 190

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
 195 200 205

Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
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Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
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Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
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 <213> Haematococcus pluvialis

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 ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg 95
 Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu
 20 25 30
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 Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala
 35 40 45
 cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg 191
 Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser
 50 55 60
 tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga 239
 Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly
 65 70 75
 acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca 287
 Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala
 80 85 90 95
 ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa 335
 Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys
 100 105 110
 cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc 383
 Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly
 115 120 125
 gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac 431
 Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His
 130 135 140
 atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc 479

Met	Thr	Val	Gly	Gly	Ala	Val	Pro	Trp	Gly	Glu	Val	Ala	Gly	Thr	Leu	
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Leu	Leu	Val	Val	Gly	Gly	Ala	Leu	Gly	Met	Glu	Met	Tyr	Ala	Arg	Tyr	
160					165					170					175	
gca	cac	aaa	gcc	atc	tgg	cat	gag	tcg	cct	ctg	ggc	tgg	ctg	ctg	cac	575
Ala	His	Lys	Ala	Ile	Trp	His	Glu	Ser	Pro	Leu	Gly	Trp	Leu	Leu	His	
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aag	agc	cac	cac	aca	cct	cgc	act	gga	ccc	ttt	gaa	gcc	aac	gac	ttg	623
Lys	Ser	His	His	Thr	Pro	Arg	Thr	Gly	Pro	Phe	Glu	Ala	Asn	Asp	Leu	
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Phe	Ala	Ile	Ile	Asn	Gly	Leu	Pro	Ala	Met	Leu	Leu	Cys	Thr	Phe	Gly	
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Phe	Trp	Leu	Pro	Asn	Val	Leu	Gly	Ala	Ala	Cys	Phe	Gly	Ala	Gly	Leu	
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ggc	atc	acg	cta	tac	ggc	atg	gca	tat	atg	ttt	gta	cac	gat	ggc	ctg	767
Gly	Ile	Thr	Leu	Tyr	Gly	Met	Ala	Tyr	Met	Phe	Val	His	Asp	Gly	Leu	
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Val	His	Arg	Arg	Phe	Pro	Thr	Gly	Pro	Ile	Ala	Gly	Leu	Pro	Tyr	Met	
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Lys	Arg	Leu	Thr	Val	Ala	His	Gln	Leu	His	His	Ser	Gly	Lys	Tyr	Gly	
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Gly	Ala	Pro	Trp	Gly	Met	Phe	Leu	Gly	Pro	Gln	Glu	Leu	Gln	His	Ile	
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Pro	Gly	Ala	Ala	Glu	Glu	Val	Glu	Arg	Leu	Val		Glu	Leu	Asp	Trp	
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Ser	Lys	Arg														
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<210> 32
<211> 322
<212> PRT
<213> Haematococcus pluvialis

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<400> 32
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Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu Ser
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Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala Arg
          35          40          45

Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu
50          55          60

Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr
65          70          75          80

Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu
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Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg
          100          105          110

Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val
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Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met
          130          135          140

Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu
145          150          155          160

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala
          165          170          175

His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys
          180          185          190

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Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe
 195 200 205

Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe
 210 215 220

Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly
 225 230 235 240

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val
 245 250 255

His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys
 260 265 270

Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly
 275 280 285

Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro
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Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser
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Lys Arg

<210> 33
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 <212> DNA
 <213> Erwinia uredovora

<220>
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 <222> (1)..(528)

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 Met Glu Val Ile Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
 20 25 30
 ggt tgg gga tgg cat ctt tca cat cat gaa ccg cgt aaa ggt gcg ttt 144
 Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
 35 40 45
 gaa gtt aac gat ctt tat gcc gtg gtt ttt gct gca tta tcg atc ctg 192

Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu
 50 55 60
 ctg att tat ctg ggc agt aca gga atg tgg ccg ctc cag tgg att ggc 240
 Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly
 65 70 75 80
 gca ggt atg acg gcg tat gga tta ctc tat ttt atg gtg cac gac ggg 288
 Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
 85 90 95
 ctg gtg cat caa cgt tgg cca ttc cgc tat att cca cgc aag ggc tac 336
 Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
 100 105 110
 ctc aaa cgg ttg tat atg gcg cac cgt atg cat cac gcc gtc agg ggc 384
 Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
 115 120 125
 aaa gaa ggt tgt gtt tct ttt ggc ttc ctc tat gcg ccg ccc ctg tca 432
 Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
 130 135 140
 aaa ctt cag gcg acg ctc cgg gaa aga cat ggc gct aga gcg ggc gct 480
 Lys Leu Gln Ala Thr Leu Arg Glu Arg His Gly Ala Arg Ala Gly Ala
 145 150 155 160
 gcc aga gat gcg cag ggc ggg gag gat gag ccc gca tcc ggg aag taa 528
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 165 170 175

<210> 34
 <211> 175
 <212> PRT
 <213> Erwinia uredovora

<400> 34

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 Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
 35 40 45
 Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu
 50 55 60
 Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly
 65 70 75 80
 Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
 85 90 95

Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
 100 105 110

Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
 115 120 125

Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
 130 135 140

Lys Leu Gln Ala Thr Leu Arg Glu Arg His Gly Ala Arg Ala Gly Ala
 145 150 155 160

Ala Arg Asp Ala Gln Gly Gly Glu Asp Glu Pro Ala Ser Gly Lys
 165 170 175

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Promoter

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 gatcaacagg attgagagag agaaaaagaa ctctgtgtcat ttatttctgt tgactgaaat 720
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acaatagcag ttgatcgtgt aacccaaaga gggtctttgt tattttgcac ttccgctttg      1080
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<210> 36
<211> 16245
<212> DNA
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<220>
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caagcctggg gataagtgcc ctgcggtatt gacacttgag gggcgcgact actgacagat      360
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cttggtgctg tttcagcttt attggcaatc acttatcatg cttggcactt gacactgcca 420

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aataaacctt cattttatgg ttcatgcac ctttggtatg cttgtcctgt gttggctatt 480
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<210> 68
<211> 1089
<212> DNA
<213> Blakeslea trispora

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<400> 68
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gatgatctta ctatcagctg ggatatttta cgtaaagcct caaagtcatt ctatactgca 180
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<210> 69
<211> 611
<212> DNA
<213> Blakeslea trispora

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<400> 69
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<210> 70
 <211> 882
 <212> DNA
 <213> *Haematococcus pluvialis*

<400> 70
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 gcagcaccac agacagagga ggcgctggga accgtgcagg ctgccggcgc gggcgatgag 180
 cacagcgccg atgtagcact ccagcagctt gaccgggcta tcgcagagcg tcgtgcccg 240
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 ccctggggta tgttcttggg tccacaggag ctgcagcaca ttccagggtg ggcggaggag 840
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<210> 71
 <211> 528
 <212> DNA
 <213> *Erwinia uredovora*

<400> 71
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 catgaaccgc gtaaagggtgc gtttgaagtt aacgatcttt atgccgtggt ttttgctgca 180
 ttatcgatcc tgctgattta tctgggcagt acaggaatgt ggccgctcca gtggattggc 240
 gcaggtatga cggcgtatgg attactctat tttatggtgc acgacgggct ggtgcatcaa 300
 cgttggccat tccgctatat tccacgcaag ggctacctca aacggttgta tatggcgcac 360
 cgtatgcata acgccgtcag gggcaaagaa ggttggtgtt cttttggctt cctctatgcg 420
 ccgccccctgt caaaacttca ggcgacgctc cgggaaagac atggcgctag agcgggcgct 480
 gccagagatg cgcagggcgg ggaggatgag cccgcataccg ggaagtaa 528

<210> 72
 <211> 762
 <212> DNA
 <213> *Nostoc sp. PCC73102*

<400> 72
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 ctgagtttat tactttccct tgacatctca aagctaaaat tttggatggt attgcctggt 180
 atactatggc aaacatTTTT atatacggga ttatttatta catctcatga tgccatgcat 240
 ggcgtagtat ttccccaaaa caccaagatt aatcatttga ttggaacatt gaccctatcc 300
 ctttatggtc ttttaccata tcaaaaacta ttgaaaaaac attggttaca ccaccacaat 360
 ccagcaagct caatagaccc ggattttcac aatggtaaac accaaagtgt ctttgcttgg 420
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 gaaccaatag ggggttatgt tcagcctcat tgtgccccaa caattagccg tcctatttgg 660
 tggtcattta tcacgtgcta tcattttggc taccacgagg aacatcacga atatcctcat 720
 atttcttggt ggcagttacc agaaatttac aaagcaaaat ga 762

<210> 73
 <211> 617

<212> DNA

<213> *Haematococcus pluvialis*

<400> 73

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cacctagggc tgttggtagg atcagggtgag gccttgacaca ttgcatgatg tactcgtcat      420
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<210> 74

<211> 1208

<212> DNA

<213> *Haematococcus pluvialis*

<400> 74

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ggcttgtctc tgaagcttgt aggaaaggca gacgctatca tggtgagagc taagaagggc      180
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gaggcagata acatcgaccc aacatcctcg agccatacta cagcataaaa ggatacgttt     1020
tctttaacag aaatttacct ttttggtatc agcacatata aaaaaaaaga aattttaagat     1080
gagtaggact tccatttctc caaaaatttt attcaatcca taaatgaatt atttttggac     1140
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<210> 75
<211> 6316
<212> DNA
<213> Blakeslea trispora

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<223> n is a, c, g, or t

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<220>
<221> misc_feature
<222> (4263)..(4263)
<223> n is a, c, g, or t

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<210> 76
 <211> 1170
 <212> DNA
 <213> *Thermus thermophilus*

<400> 76
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<210> 77
 <211> 2981
 <212> DNA
 <213> *Blakeslea trispora*

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<210> 78

<211> 1749

<212> DNA

<213> *Blakeslea trispora*

<400> 78

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<213> Artificial Sequence

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<220>
<223> Primer

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<400> 79
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<210> 80
<211> 25
<212> DNA
<213> Artificial Sequence

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<220>
<223> Primer

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<400> 80
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